AMENDMENTS TO THE CLAIMS

Please cancel claims 8 and 24-34, without prejudice, and amend claims 1, 9, 18, 19, 20, 22, and 23 as follows:

1. **(Currently amended)** A method for identifying a non-peptide compound that binds to a target, the method comprising:

a) forming a first library comprising a multiplicity of peptides;

b) selecting from the first library at least one peptide that binds to the target;

c) determining the amino acid sequence or sequences of the at least one peptide that binds to the target, thereby generating a peptide motif;

d) forming a second library comprising a multiplicity of non-peptide compounds designed based on the peptide motif;

e) selecting from the second library at least one non-peptide compound that binds to the target; and

f) determining the structure or structures of the at least one non-peptide compound that binds to the target;

thereby identifying a non-peptide compound that binds to the target.

2. **(Original)** The method of claim 1, wherein the first library is a phage display library.

3. **(Original)** The method of claim 1, wherein the first library is bound to a solid-support.

4. **(Original)** The method of claim 1, wherein the first library is an anchor library.

5. **(Original)** The method of claim 1, wherein the first library comprises at least about 10^6 peptides.

6. **(Original)** The method of claim 1, wherein the first library comprises at least about 10^9 peptides.

7. **(Original)** The method of claim 1, wherein the first library comprises at least about 10^{12} peptides.

8. **(Canceled)**

9. **(Original)** The method of claim 1, wherein step c) comprises determining the amino acid sequence or sequences of the at least one peptide.

10. **(Original)** The method of claim 1, wherein the second library comprises at least one peptide derivative.

11. **(Original)** The method of claim 1, wherein the second library comprises at least one peptide analogue.

12. **(Original)** The method of claim 1, wherein the second library comprises at least one peptidomimetic.

13. **(Original)** The method of claim 1, wherein the second library comprises at least about 10^2 non-peptide compounds.

14. **(Original)** The method of claim 1, wherein the second library comprises at least about 10^4 non-peptide compounds.

15. **(Original)** The method of claim 1, wherein the second library comprises at least about 10^6 non-peptide compounds.

16. **(Original)** The method of claim 1, wherein step f) comprises analyzing the at least one non-peptide compound by a mass spectrometric method.

17. **(Original)** The method of claim 16, wherein the mass spectrometric method comprises tandem mass spectrometry.

18. **(Currently amended)** The method of claim 1, wherein the non-peptide compound that binds to a target has a binding affinity for the target of at least about 10^{-7} M.

19. **(Currently amended)** The method of claim 1, wherein the non-peptide compound that binds to a target has a binding affinity for the target of at least about 10^{-8} M.

20. **(Currently amended)** The method of claim 1, wherein the non-peptide compound that binds to a target has a binding affinity for the target of at least about 10^{-9} M.

21. **(Original)** The method of claim 1, further comprising:

g) forming a third library comprising a multiplicity of non-peptide compounds designed based on the structure or structures of the non-peptide compound or compounds determined in step f);

h) selecting from the third library at least one non-peptide compound that binds to the target; and

i) determining the structure or structures of the at least one non-peptide compound selected in step h);

thereby identifying a compound that binds to the target.

22. **(Currently amended)** A method for identifying a non-peptide compound that binds to a target, the method comprising:

a) forming a first library comprising a multiplicity of peptides displayed on the surface of a bacteriophage;

b) selecting from the first library at least one peptide that binds to the target;

c) determining the sequence or sequences of the at least one peptide that binds to the target, thereby generating a peptide motif;

d) forming a second library comprising a multiplicity of non-peptide compounds designed based on the peptide motif;

e) selecting from the second library at least one non-peptide compound that binds to the target; and

f) determining the structure or structures of the at least one non-peptide compound that binds to the target by tandem mass spectrometry;

thereby identifying a non-peptide compound that binds to the target.

23. **(Currently amended)** A method for identifying a non-peptide compound that binds to a target, the method comprising:

a) forming a first library comprising an anchor library of a multiplicity of peptides;

b) selecting from the first library at least one peptide that binds to the target;

c) determining the sequence or sequences of the at least one peptide that binds to the Target, thereby generating a peptide motif;

d) forming a second library comprising a multiplicity of non-peptide compounds designed based on the peptide motif;

e) selecting from the second library at least one non-peptide compound that binds to the target; and

f) determining the structure or structures of the at least one non-peptide compound that binds to the target by tandem mass spectrometry;

thereby identifying a non-peptide compound that binds to the target.

24. (Canceled)
25. (Canceled)
26. (Canceled)
27. (Canceled)
28. (Canceled)
29. (Canceled)
30. (Canceled)
31. (Canceled)
32. (Canceled)
33. (Canceled)
34. (Canceled)